## Fig. 1

>Score	= 38.1				
	QPSPSGAAVNSSESLPPSSSVNDISSMSTDQTL QSSATFSTAATSVSSSASSGVSLSSSMNTANSL QSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	(SEQ (SEQ			-
>Score	= 35.3				
		(SEQ (SEQ			
>Score	= 25.7				·
	QGFDKQ QTFDKQ Q FDKQ	(SEQ (SEQ (SEQ	ID	NO:	12)
>Score	= 26.1				
	HSAGIIHRDLKPSN HPTTTTSWDLKPPT H DLKP	(SEQ (SEQ (SEQ	ID	NO:	27)
>Score	= 26.1				
	PSGAAVNSSESLPPSSSVNDISSMSTDQTL PYQSPVSSSES-APGTIMNGHGGGRSQQTL P V SSES P N QTL	(SEQ (SEQ (SEQ	ID	NO:	30)
>Score	= 25.8				
		(SEQ (SEQ			
>Score	= 26.5				
	PSPSGAAVNSSESLPPSSSVNDISSMSTDQTLAS-DTDSSLEASA SSPLSQLSSSLSSHQSSLSAHAALSSSTSHTHASVESASSHQSSA SP S S S S S T T AS SS SA	(SEQ			

Fig. 2

 $u = \frac{1}{\delta^2}, \quad u = 0$ 

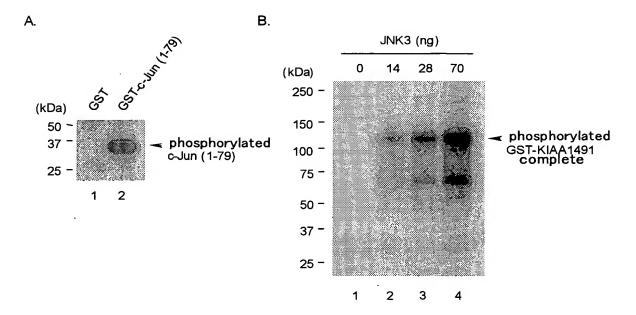
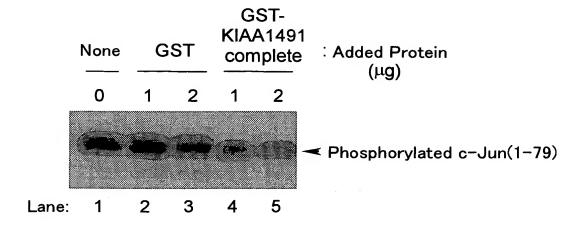


Fig. 3



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_	•		4
н	1	σ	4
	•	5.	

15.	1				
>Şc	ore	= 35.0			
1		QPSPSGAAVNSSESLPPSSSVNDISSMSTDQ QPPPPEKTPNPMECTKPGAALSQDSAVSLEQ QP P N E P S S Q	(SEQ (SEQ		
>Sc	ore	= 25.9			
		FTPQKTLEE YSLQQTLDE Q TL E	(SEQ (SEQ		•
>Sc	ore	= 26.4			
		SDCTLKILDFGLARTAGTSF SDKNLSIFDFSSGECVATMF SD L I DF T F	(SEQ (SEQ		
>Sc	core	= 25.6			
	_	KLKASQARDLLSKML KLLASASRDRLIHVL KL AS RD L L	(SEQ (SEQ		
>Sc	core	= 25. 2			
		SLFPADSEHNKLKASQARDLLSK SLVPQERHEASLQAPSPGALLSR SL P A LLS	(SEQ (SEQ		
>Sc	core	= 25.9			
		IEEWKEL-IYKEVMNSEE LDKWVELRVYPEVKDSNQ W EL Y EV S	(SEQ (SEQ		
>Sc	ore	= 26.7			
		SSMSTDQTLASDTD SMLSPGPALSSDSD S S L SD D	(SEQ (SEQ		

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Fig. 5

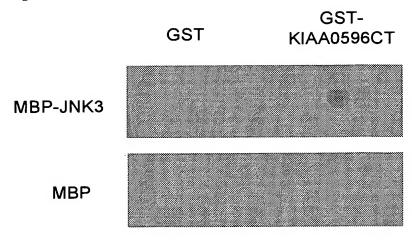


Fig. 6

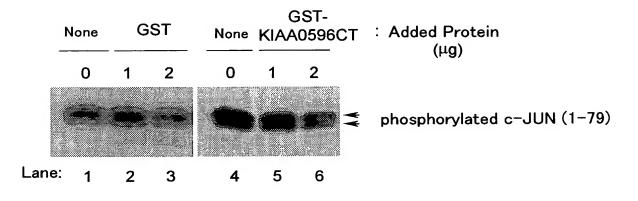


Fig. 7		
>Score	= 28.2	
	SKSKVDNQFYSVEVGDSTFTVLK TREKITTNCYKFKIKDGSFITLR K Y D F L	(SEQ ID NO: 50) (SEQ ID NO: 51)
>Score	= 28.0	
	VGDSTFTVLKRYQN VSESVFKILNYSQN V S F L QN	(SEQ ID NO: 52) (SEQ ID NO: 53)
>Score	= 28.8	
	EQLGTPCPEF ELLGTSCYEY E LGT C E	(SEQ ID NO: 54) (SEQ ID NO: 55)
>Score	= 26.1	
	SSMSTDQTLASDTDSSLEASAG SSPSNDEAAMAVIMSLLEADAG SS S D S LEA AG	(SEQ ID NO: 56) (SEQ ID NO: 57)
>Score	= 25.6	
	SDCTLKILDF SESVFKILNY S KIL	(SEQ ID NO: 58) (SEQ ID NO: 59)
>Score	= 26.1	
	YIDQWNKVIE FMNPWTKEVE W K E	(SEQ ID NO: 60) (SEQ ID NO: 61)
>Score	= 25.2	
	VKGQPSPSGAA VKEQLSSSDTA	(SEQ ID NO: 62) (SEQ ID NO: 63)

161 VKEQLSSSDTA VK Q S S A

Fig.8	
>Score =	31.4

402	<b>EEKTKNGV</b>	VKGQPSPSG	AAVNSSESI	LPPSSS	(SEQ	ID	NO:	64)
503	<b>DDSSPTGL</b>	MKDTHTVNC	RSMSNKELI	FPPSPS	(SEQ	ID	NO:	65)
	G	K	F	PPS S				

>Score = 28.8

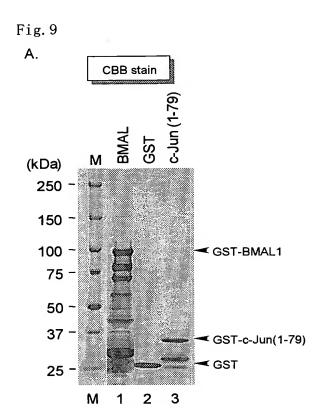
277 EQLGTPCPEF	(SEQ ID NO: 66)
364 ELLGTSCYEY	(SEQ ID NO: 67)
E LGT C E	

>Score = 27.0

40	SKSKVDNO	FYSVE	VGDS	TFT	VLK	(SEQ	ID I	: ON	68)
392	SKEKILTE	SYKFR	<b>AKDG</b>	SFV	TLK	(SEQ	ID!	NO:	69)
	CK K	V	ח	F	I K				

>Score = 25.4

40	SKSKVDNQFYSV	(SEQ	ID	NO:	70)
269	SKKKEHRKFYTI	(SEQ	ID	NO:	71)
	SK K FY				



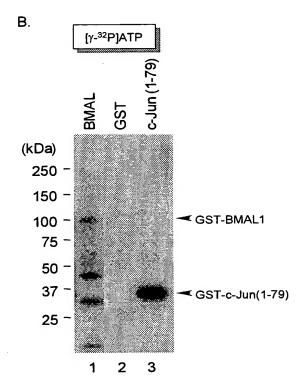


Fig. 10

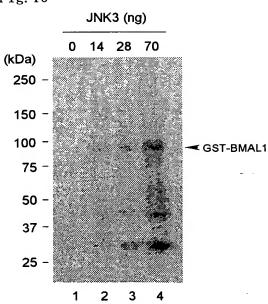


Fig. 11

	None	GST		None	GST- BMAL1		: Added Protein (μg)
	0	1	2	0	1	2	♣ Phosphorylated c-Jun (1-79)
Lane	»: 1	2	3	4	5	6	

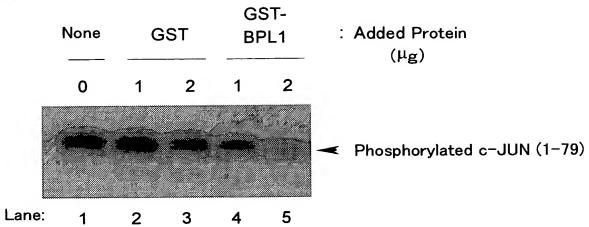
Fig. 12		
>Score	= 30.9	
	SYLLYQML SYILYHLL SY LY L	(配列番号72) (配列番号73)
>Score	= 27.7	
	SEPTLDVK PEPSLEIK EP L K	(配列番号74) (配列番号75)
>Score	= 28.2	
	IHRDLKPSNIVVKS VHLELPPSSNIVQT H L PS V	(配列番号76) (配列番号77)
>Score	= 26.2	
	QKTLEEFQD EKLIKEFQD K EFQD	(配列番号78) (配列番号79) (配列番号80)
>Score	= 26.8	
	DANLCQVIQMEL EAVLCQV-HLEL A LCQV EL	(SEQ ID NO: 81) (SEQ ID NO: 82) (SEQ ID NO: 83)
>Score	= 27.1	
	LPPSSSV LPPSSNI LPPSS	(SEQ ID NO: 84) (SEQ ID NO: 85) (SEQ ID NO: 86)
>Score	= 25.1	
	POKTLEEFODVYLVM SQEALGRFHEVRSVL Q L F V V	(SEQ ID NO: 87) (SEQ ID NO: 88)

(SEQ ID NO: 89) (SEQ ID NO: 90)

>Score = 25.1

134 KTLEEFQDVYL 576 RSIPEYQDINL E QD L 10/10

Fig. 13



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